



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 10:15 AM UTC

PDB ID : 7M30 / pdb_00007m30
EMDB ID : EMD-23640
Title : Cryo-EM structure of the HCMV pentamer bound by antibodies 1-103, 1-32 and 2-25
Authors : Wrapp, D.; McLellan, J.S.
Deposited on : 2021-03-17
Resolution : 3.81 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

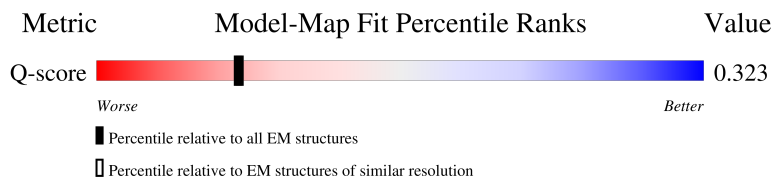
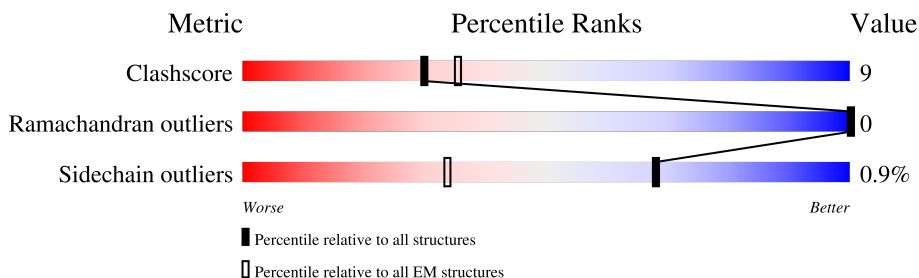
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.81 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	9193 (3.31 - 4.31)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	248	
2	C	144	
3	D	189	
4	E	111	

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Mol	Chain	Length	Quality of chain
5	F	234	
6	G	212	
7	H	241	
8	L	213	
9	M	232	
10	N	210	

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 9191 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Envelope glycoprotein L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	84	Total	C	N	O	S	0	0
			657	413	110	129	5		

- Molecule 2 is a protein called Envelope protein UL128.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	135	Total	C	N	O	S	0	0
			1090	683	197	199	11		

- Molecule 3 is a protein called Envelope glycoprotein UL130.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	170	Total	C	N	O	S	0	0
			1384	885	239	252	8		

- Molecule 4 is a protein called UL131A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	108	Total	C	N	O	S	0	0
			893	557	168	166	2		

- Molecule 5 is a protein called 2-25 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	121	Total	C	N	O	S	0	0
			947	595	163	184	5		

- Molecule 6 is a protein called 2-25 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	108	Total	C	N	O	S	0	0
			818	506	135	174	3		

- Molecule 7 is a protein called 1-32 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	114	Total	C	N	O	S	0	0
			872	545	161	160	6		

- Molecule 8 is a protein called 1-32 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L	106	Total	C	N	O	S	0	0
			813	513	130	167	3		

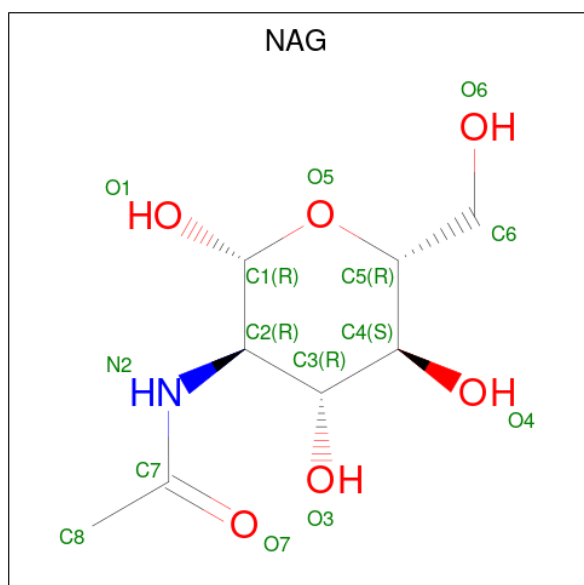
- Molecule 9 is a protein called 1-103 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	M	119	Total	C	N	O	S	0	0
			914	580	154	178	2		

- Molecule 10 is a protein called 1-103 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	102	Total	C	N	O	S	0	0
			775	484	132	157	2		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

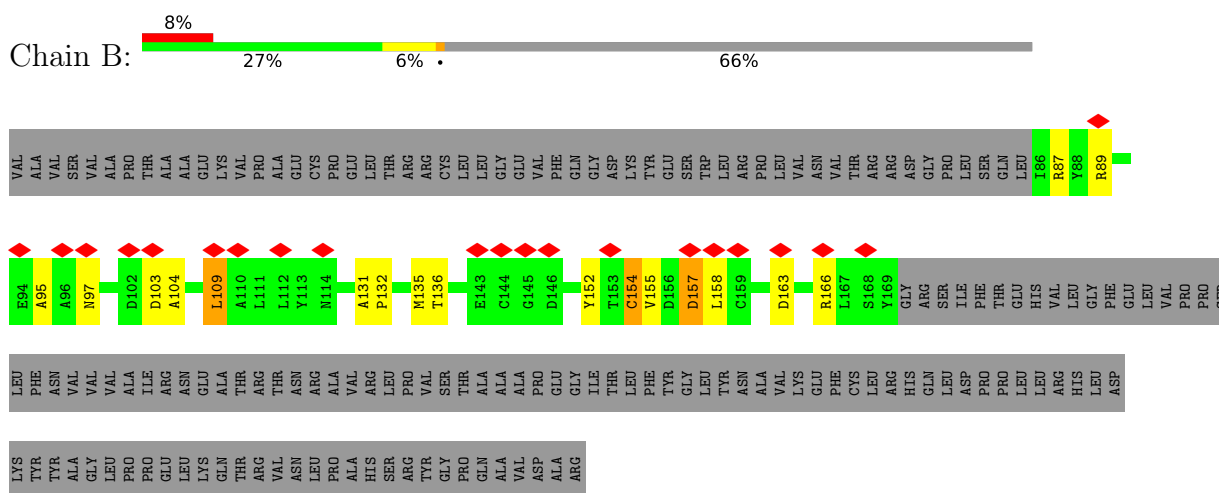


Mol	Chain	Residues	Atoms				AltConf
11	D	1	Total	C	N	O	0
			14	8	1	5	
11	E	1	Total	C	N	O	0
			14	8	1	5	

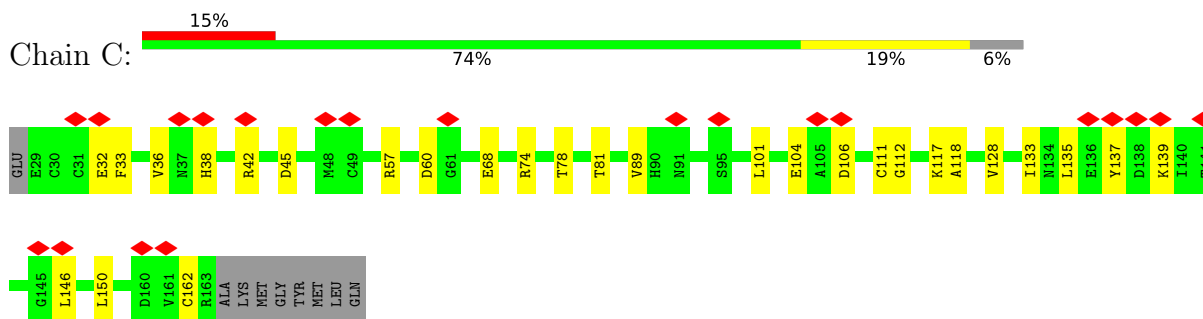
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

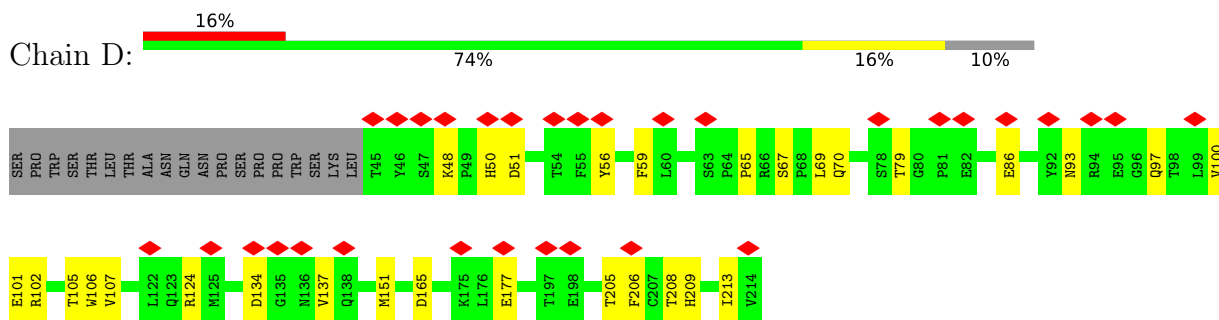
- Molecule 1: Envelope glycoprotein L



- Molecule 2: Envelope protein UL128

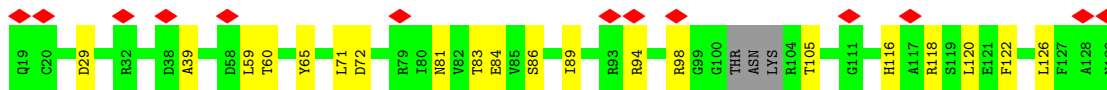
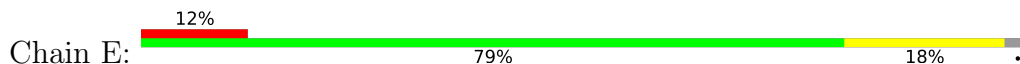


- Molecule 3: Envelope glycoprotein UL130



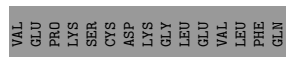
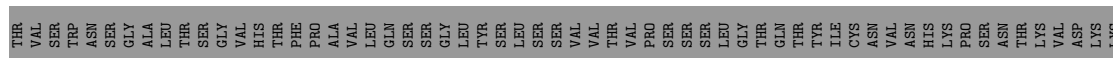
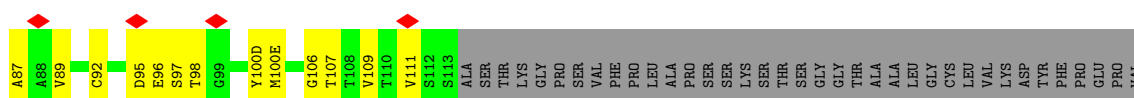
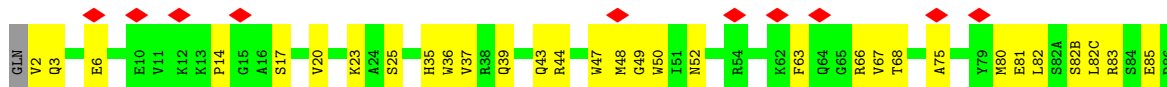
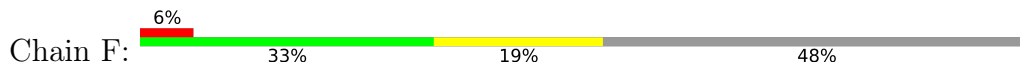
- Molecule 4: UL131A

Chain E:



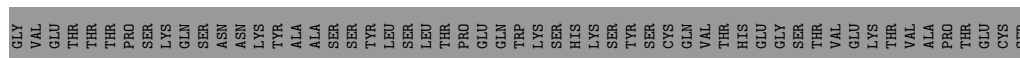
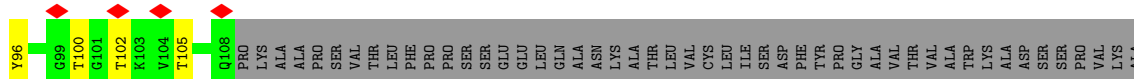
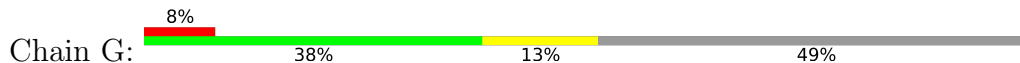
- Molecule 5: 2-25 Fab Heavy Chain

Chain F:



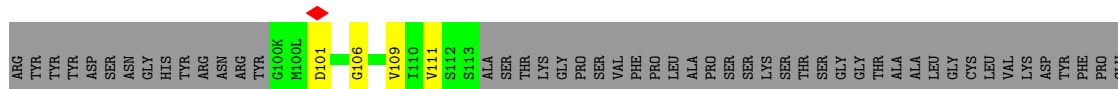
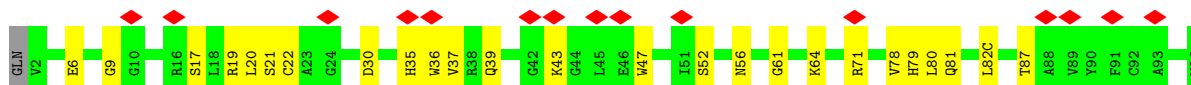
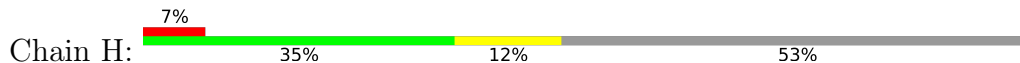
- Molecule 6: 2-25 Fab Light Chain

Chain G:



- Molecule 7: 1-32 Fab Heavy Chain

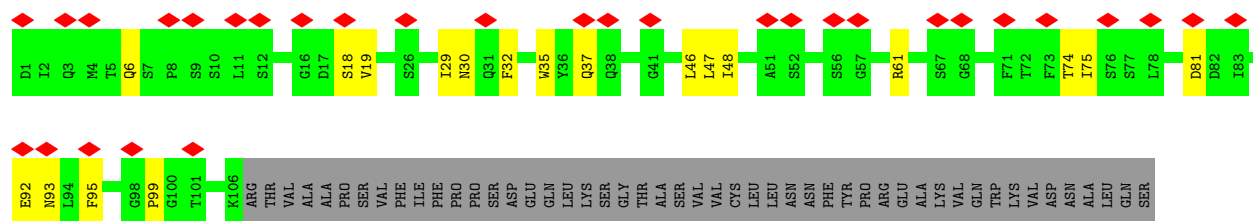
Chain H:



LYS
LYS
VAL
GLU
PRO
LYS
SER
CYS
ASP
LYS
GLY
LEU
GLU
VAL
LEU
PHE
GLN

• Molecule 8: 1-32 Fab Light Chain

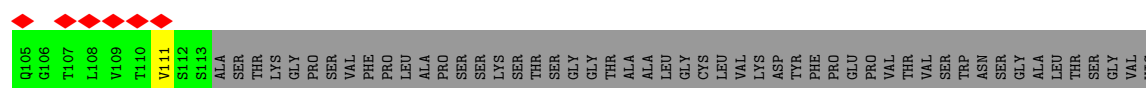
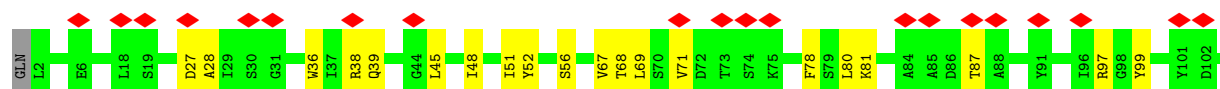
Chain L: 15% 41% 9% 50%



GLY
ASN
SER
GLN
GLU
SER
VAL
THR
GLU
GLN
ASP
SER
LYS
ASP
SER
THR
VAL
THR
ALA
ALA
SER
LEU
SER
SER
PHE
THR
ILE
PHE
PRO
PRO
LEU
SER
SER
ASP
ALA
GLU
GLN
TYR
LEU
GLY
HIS
LYS
THR
ALA
VAL
SER
VAL
CYS
GLU
VAL
THR
HIS
ASN
GLN
PHE
TYR
LEU
SER
PRO
ARG
GLY
VAL
CYS

• Molecule 9: 1-103 Fab Heavy Chain

Chain M: 11% 42% 9% 49%

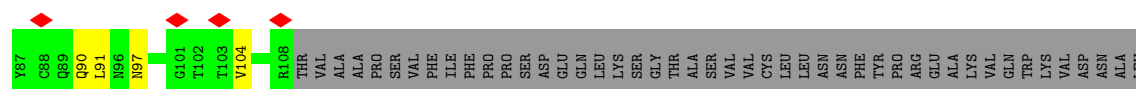
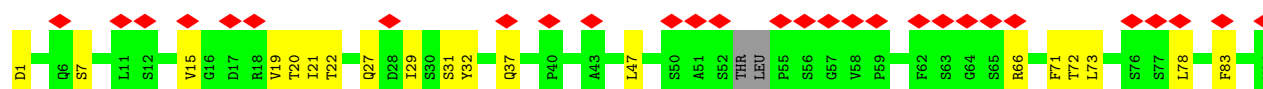


THR
PHE
PRO
ALA
VAL
LEU
GLN
SER
GLY
TYR
SER
LEU
SER
VAL
VAL
THR
VAL
PRO
SER
SER
SER
SER
GLY
THR
THR
THR
ILE
CYS
ASN
LYS
VAL
ASN
HIS
LYS
HIS
GLY
LEU
VAL
SER
ASN
THR
LYS
VAL
PHE
ASP
LYS
LYS
VAL
VAL
GLU
THR
PRO
LYS
SER
CYS
SER
TRP
LYS
PHE
ASN
SER
GLY
ALA
LEU
THR
SER
GLY
VAL
PHE

GLN

• Molecule 10: 1-103 Fab Light Chain

Chain N: 15% 38% 11% 51%



GLN
SER
GLY
ASN
SER
GLN
GLU
SER
VAL
THR
GLU
GLN
ASP
SER
LYS
ASP
SER
THR
ALA
PRO
SER
VAL
SER
PHE
THR
ILE
PHE
THR
PRO
LEU
SER
SER
LYS
ASP
ALA
GLU
GLN
LYS
SER
HIS
LYS
VAL
TYR
CYS
VAL
THR
HIS
ASN
GLN
GLY
LEU
SER
SER
SER
PRO
VAL
THR
LYS
VAL
PHE
TRP
LYS
VAL
ARG
GLY
ASP
ASN
ALA
CYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	198946	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.054	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.476	Depositor
Map size (Å)	464.40002, 464.40002, 464.40002	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.075, 1.075, 1.075	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	B	0.31	0/670	0.87	5/916 (0.5%)
2	C	0.26	0/1112	0.80	0/1503
3	D	0.25	0/1423	0.67	0/1935
4	E	0.26	0/912	0.61	0/1233
5	F	0.24	0/969	0.65	0/1312
6	G	0.22	0/836	0.56	0/1140
7	H	0.25	0/890	0.66	0/1200
8	L	0.26	0/833	0.61	0/1133
9	M	0.23	0/938	0.62	0/1278
10	N	0.31	0/791	0.69	1/1074 (0.1%)
All	All	0.26	0/9374	0.68	6/12724 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	N	97	ASN	N-CA-C	7.77	120.78	110.53
1	B	154	CYS	N-CA-C	6.57	119.31	108.99
1	B	157	ASP	N-CA-C	5.87	117.75	111.36
1	B	131	ALA	CA-C-N	5.23	139.54	127.00
1	B	131	ALA	C-N-CA	5.23	139.54	127.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	657	0	638	19	0
2	C	1090	0	1075	20	0
3	D	1384	0	1351	24	0
4	E	893	0	851	15	0
5	F	947	0	905	32	0
6	G	818	0	767	19	0
7	H	872	0	849	21	0
8	L	813	0	775	15	0
9	M	914	0	882	15	0
10	N	775	0	753	15	0
11	D	14	0	13	1	0
11	E	14	0	13	0	0
All	All	9191	0	8872	164	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 164 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:158:LEU:HD23	3:D:56:TYR:CD2	1.84	1.11
1:B:158:LEU:HD11	3:D:100:VAL:HB	1.29	1.08
5:F:95:ASP:OD1	5:F:100(D):TYR:O	1.71	1.08
1:B:158:LEU:HD21	3:D:100:VAL:HG11	1.43	1.00
10:N:15:VAL:HA	10:N:78:LEU:HD22	1.63	0.81

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	82/248 (33%)	73 (89%)	9 (11%)	0	100	100
2	C	133/144 (92%)	122 (92%)	11 (8%)	0	100	100
3	D	168/189 (89%)	158 (94%)	10 (6%)	0	100	100
4	E	104/111 (94%)	98 (94%)	6 (6%)	0	100	100
5	F	119/234 (51%)	115 (97%)	4 (3%)	0	100	100
6	G	106/212 (50%)	103 (97%)	3 (3%)	0	100	100
7	H	110/241 (46%)	105 (96%)	5 (4%)	0	100	100
8	L	104/213 (49%)	97 (93%)	7 (7%)	0	100	100
9	M	117/232 (50%)	115 (98%)	2 (2%)	0	100	100
10	N	98/210 (47%)	94 (96%)	4 (4%)	0	100	100
All	All	1141/2034 (56%)	1080 (95%)	61 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	73/212 (34%)	71 (97%)	2 (3%)	39	59
2	C	122/129 (95%)	119 (98%)	3 (2%)	42	61
3	D	156/174 (90%)	154 (99%)	2 (1%)	61	71
4	E	95/98 (97%)	95 (100%)	0	100	100
5	F	99/197 (50%)	99 (100%)	0	100	100
6	G	91/181 (50%)	90 (99%)	1 (1%)	65	73
7	H	91/202 (45%)	91 (100%)	0	100	100
8	L	94/190 (50%)	94 (100%)	0	100	100
9	M	101/199 (51%)	100 (99%)	1 (1%)	68	74
10	N	89/186 (48%)	89 (100%)	0	100	100
All	All	1011/1768 (57%)	1002 (99%)	9 (1%)	68	74

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	G	46	LEU
9	M	69	LEU
2	C	111	CYS
2	C	162	CYS
3	D	105	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
6	G	37	GLN
6	G	50	GLN
10	N	90	GLN
9	M	39	GLN
10	N	79	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	NAG	E	200	4	14,14,15	0.29	0	17,19,21	0.68	1 (5%)
11	NAG	D	300	3	14,14,15	0.37	0	17,19,21	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	NAG	E	200	4	-	2/6/23/26	0/1/1/1
11	NAG	D	300	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	E	200	NAG	C1-O5-C5	2.30	115.27	112.19

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	E	200	NAG	O5-C5-C6-O6
11	E	200	NAG	C4-C5-C6-O6
11	D	300	NAG	O5-C5-C6-O6
11	D	300	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	D	300	NAG	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

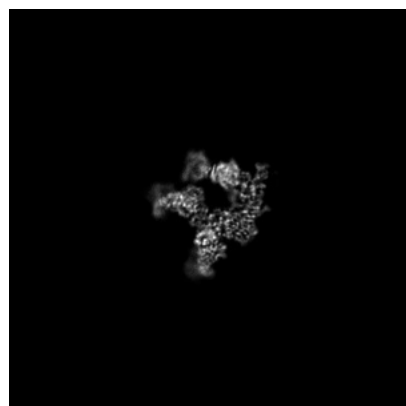
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23640. These allow visual inspection of the internal detail of the map and identification of artifacts.

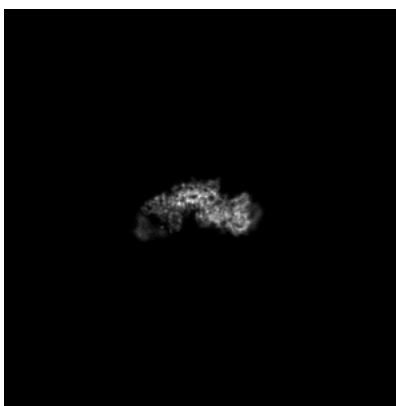
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

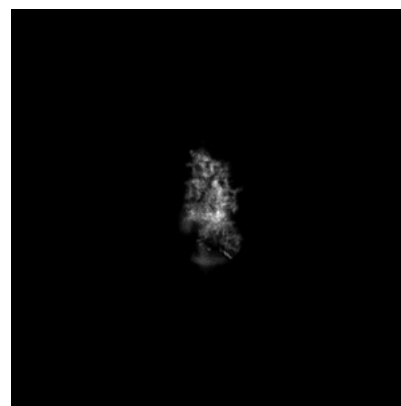
6.1.1 Primary map



X

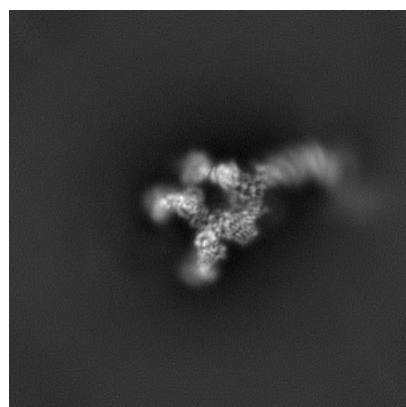


Y

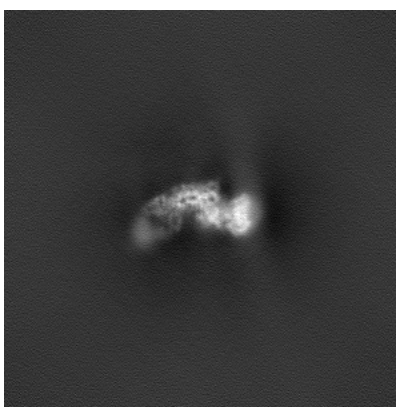


Z

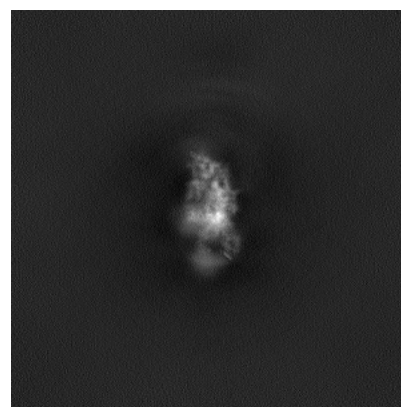
6.1.2 Raw map



X



Y



Z

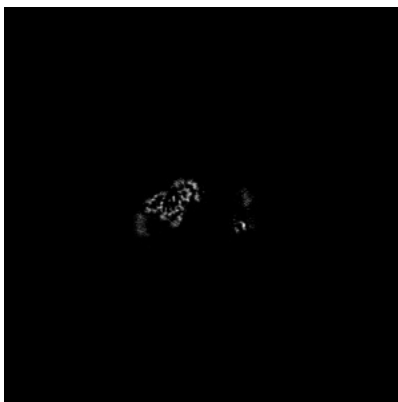
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

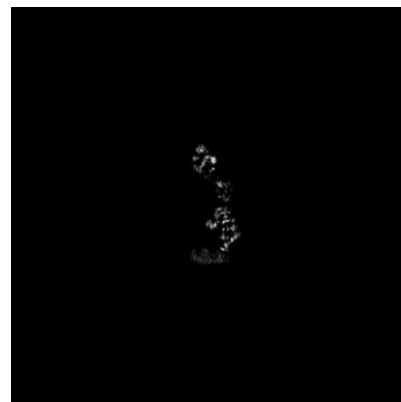
6.2.1 Primary map



X Index: 216



Y Index: 216

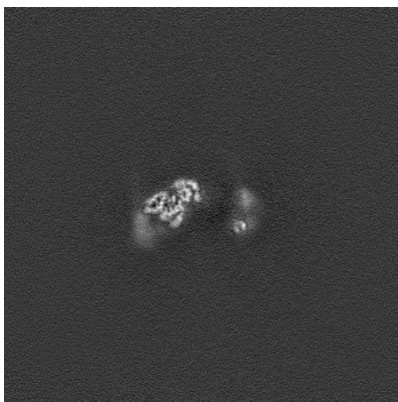


Z Index: 216

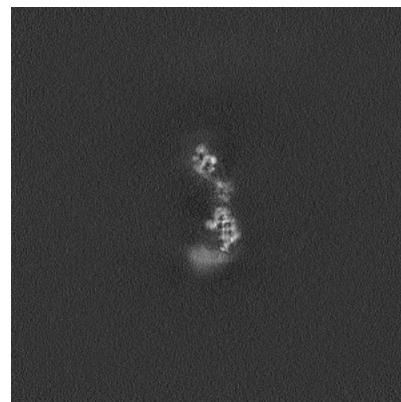
6.2.2 Raw map



X Index: 216



Y Index: 216



Z Index: 216

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 223



Y Index: 210

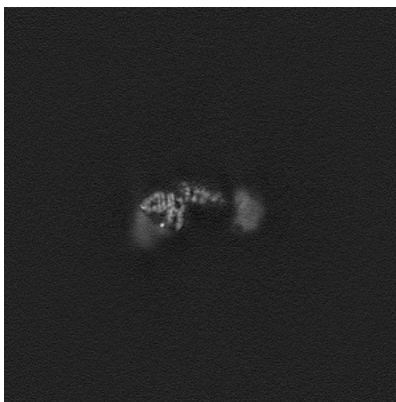


Z Index: 220

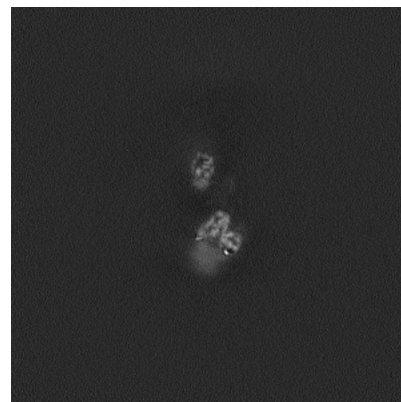
6.3.2 Raw map



X Index: 223



Y Index: 210

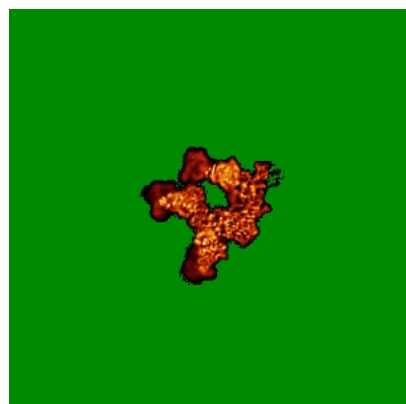


Z Index: 228

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

6.4.1 Primary map



X

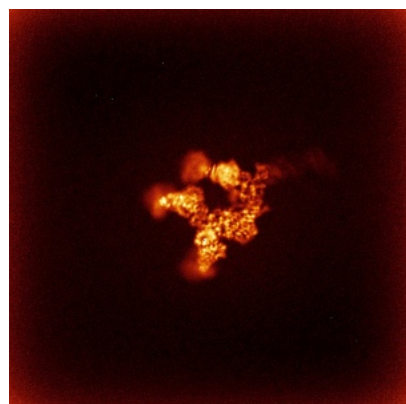


Y

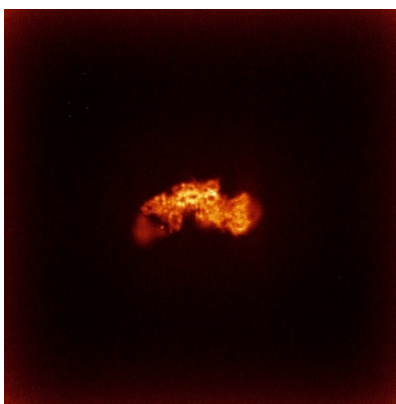


Z

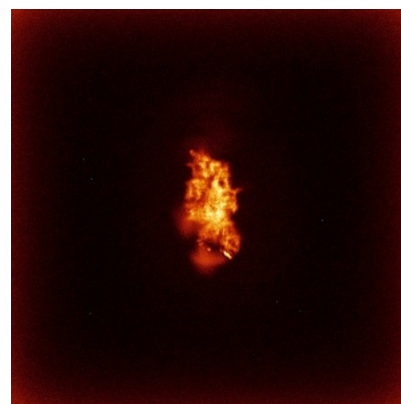
6.4.2 Raw map



X



Y

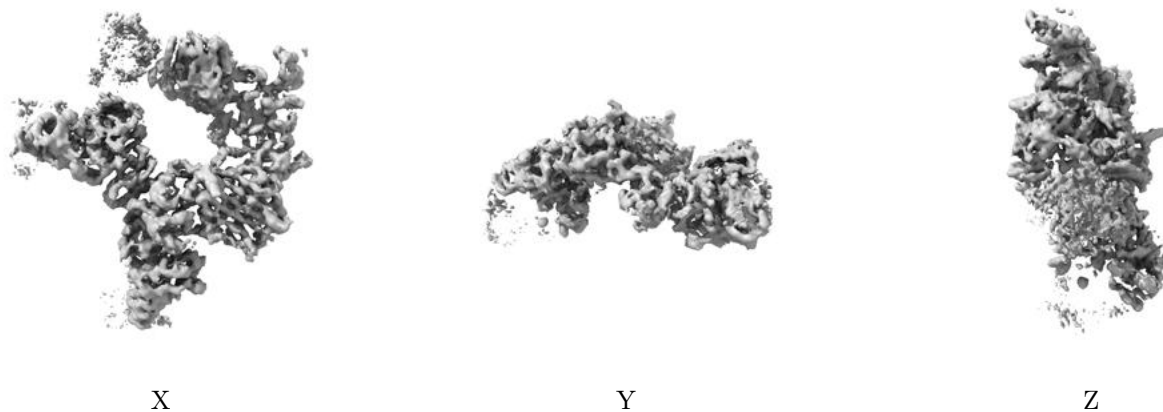


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

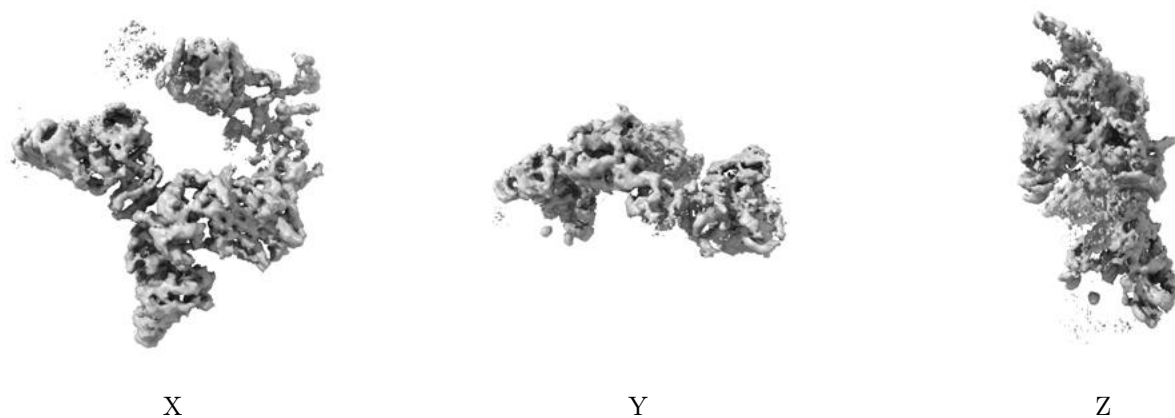
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.476. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

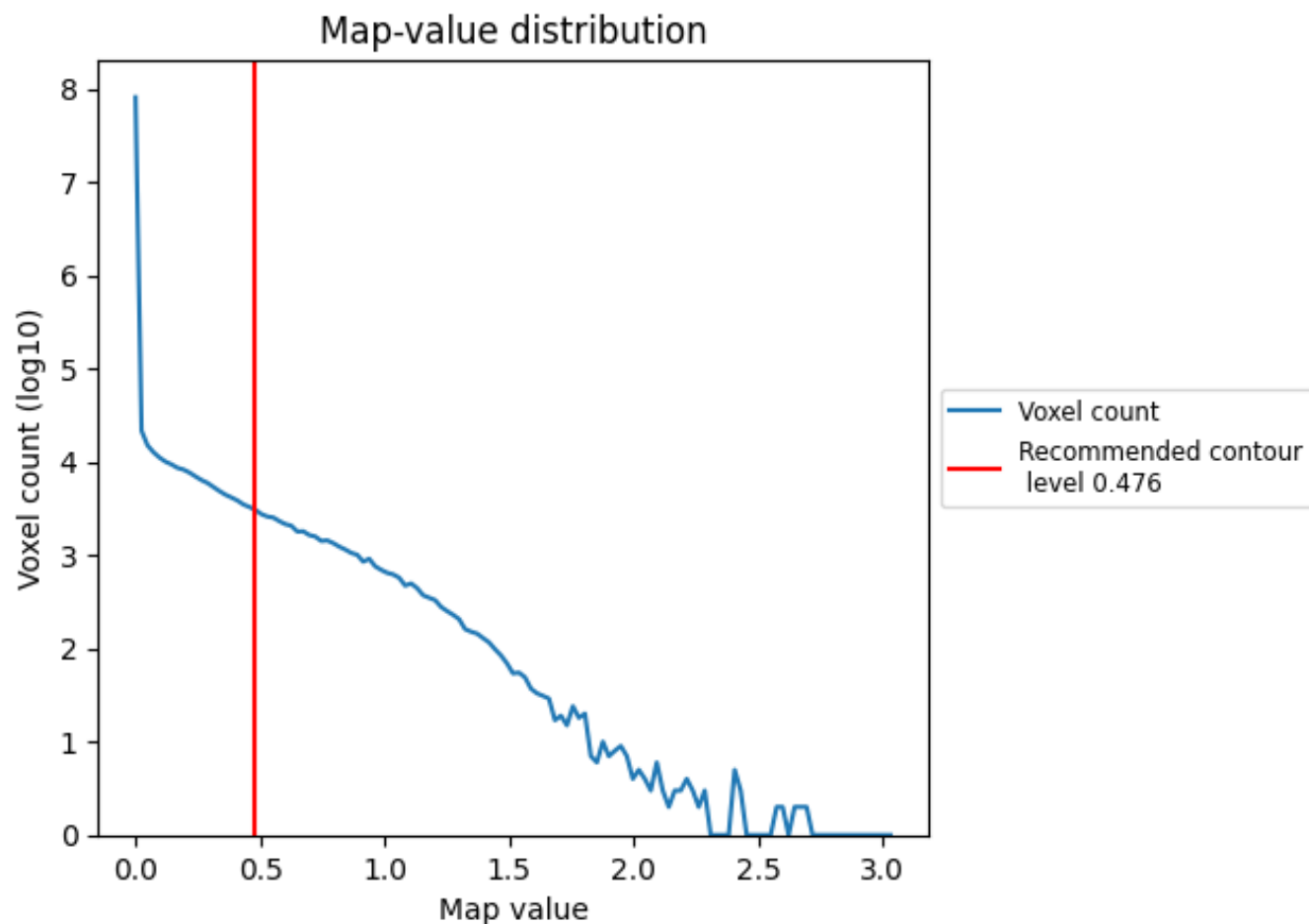
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

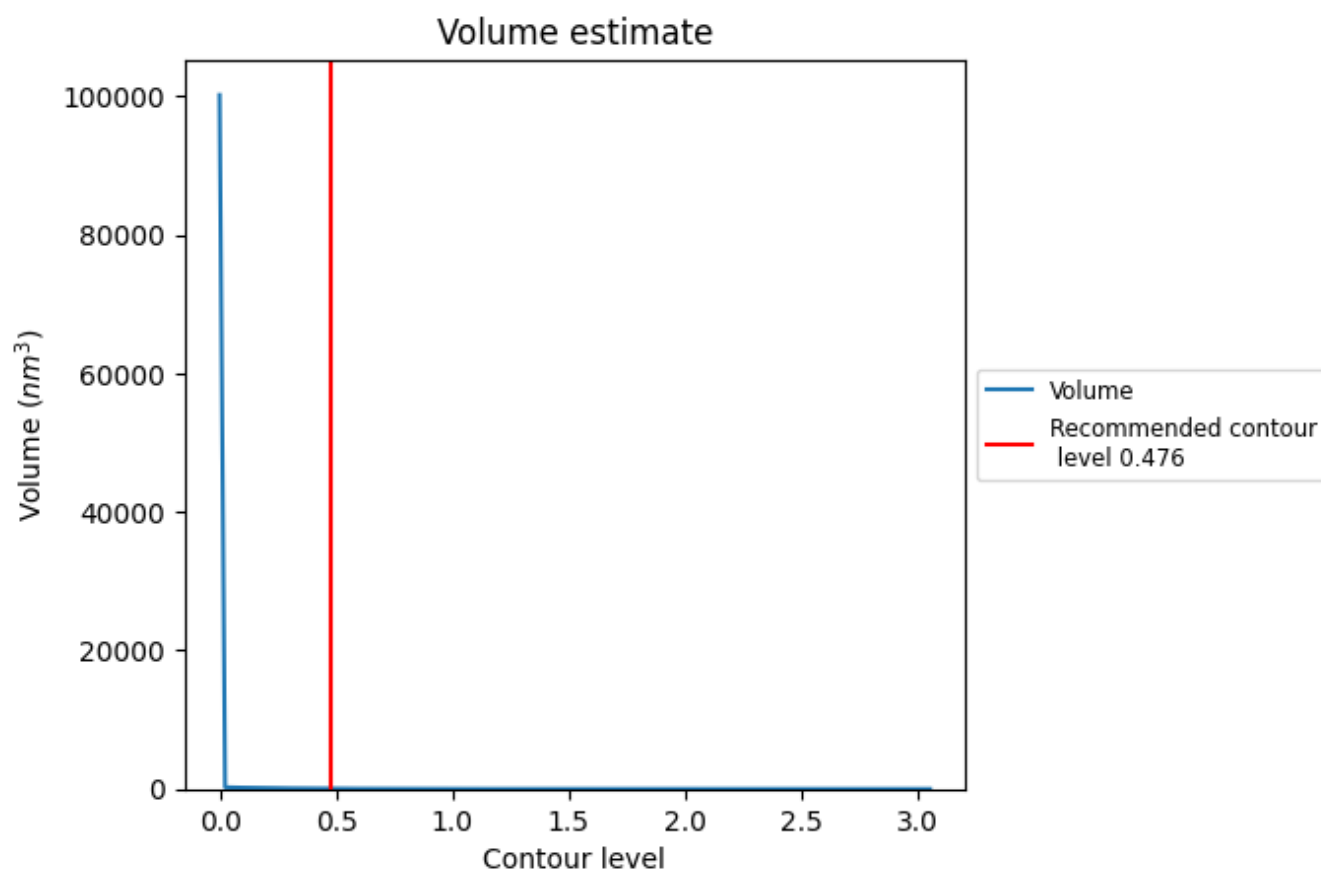
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

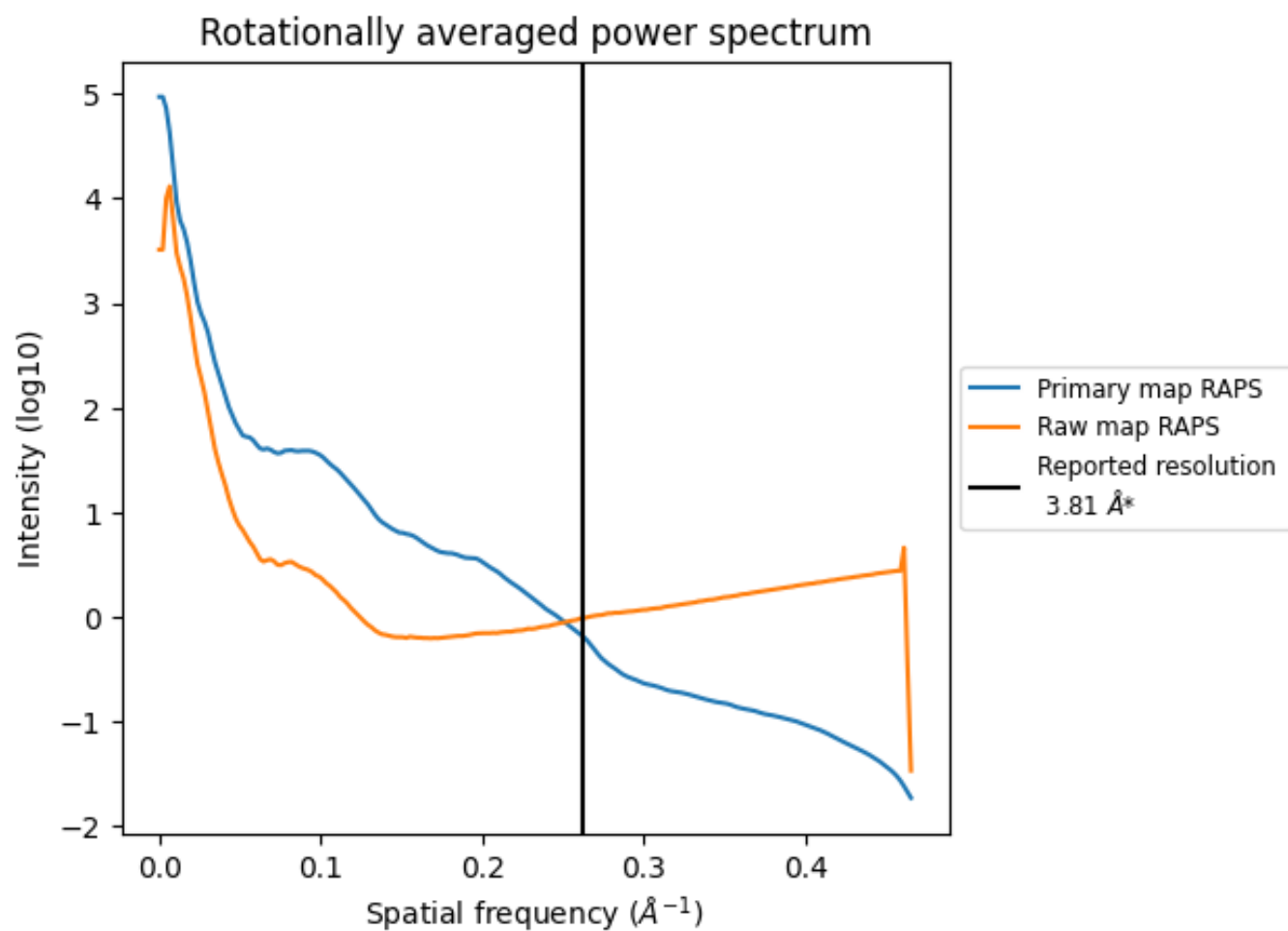
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 54 nm^3 ; this corresponds to an approximate mass of 49 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

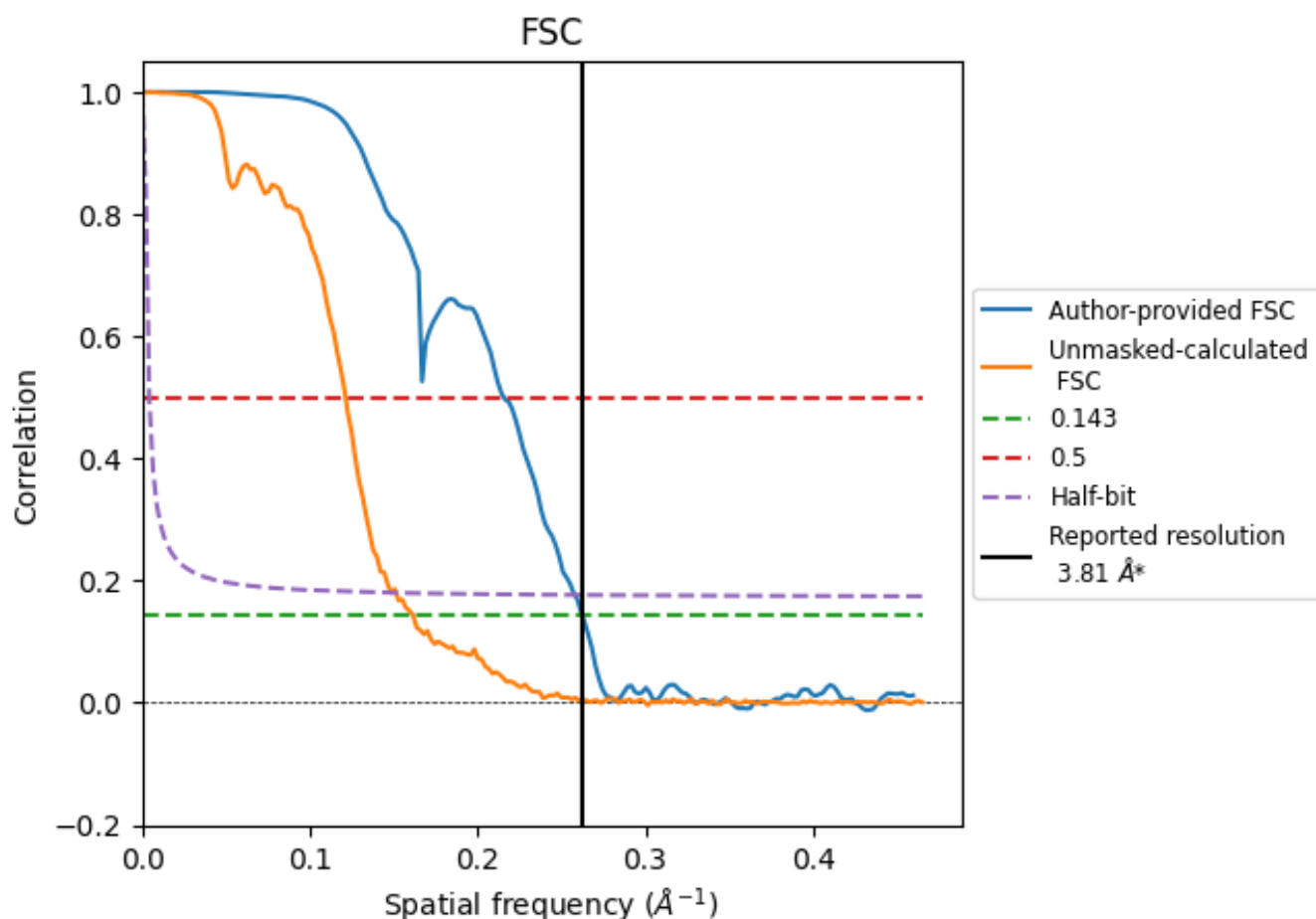


*Reported resolution corresponds to spatial frequency of 0.262 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.262 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

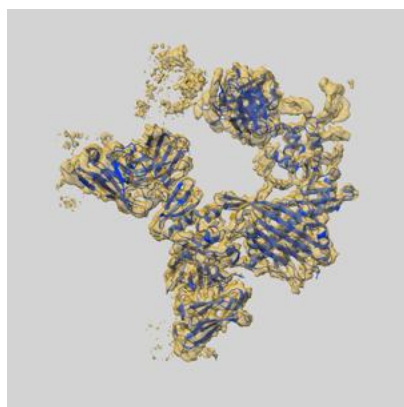
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.81	-	-
Author-provided FSC curve	3.81	4.64	3.88
Unmasked-calculated*	6.19	8.24	6.73

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.19 differs from the reported value 3.81 by more than 10 %

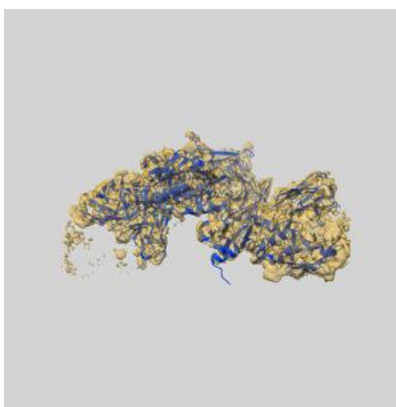
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23640 and PDB model 7M30. Per-residue inclusion information can be found in section [3](#) on page [7](#).

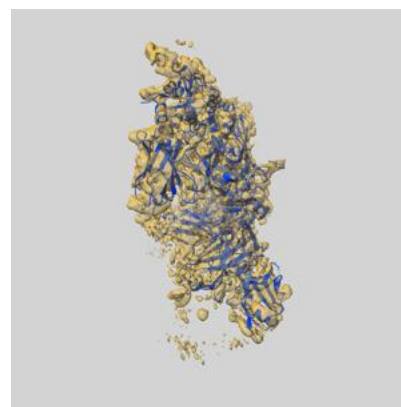
9.1 Map-model overlay [i](#)



X



Y



Z

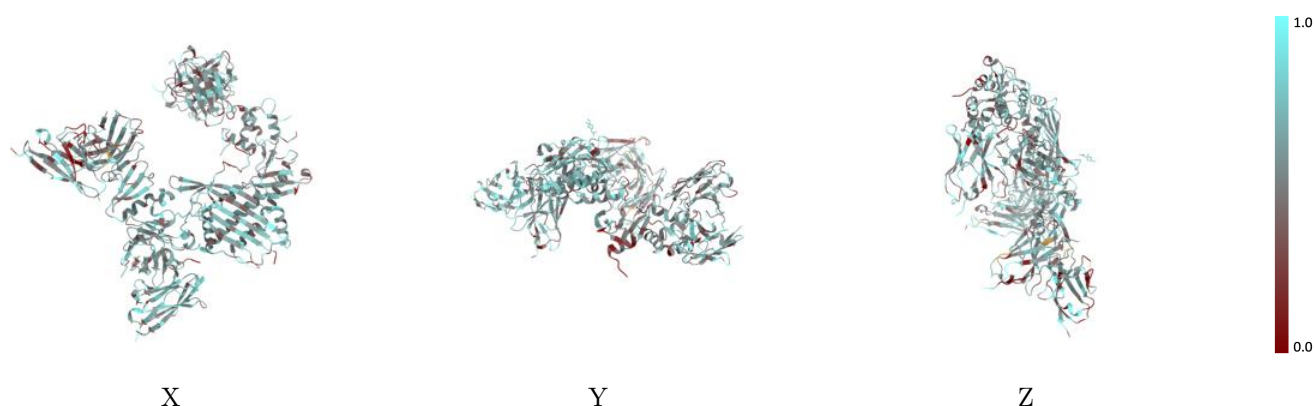
The images above show the 3D surface view of the map at the recommended contour level 0.476 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



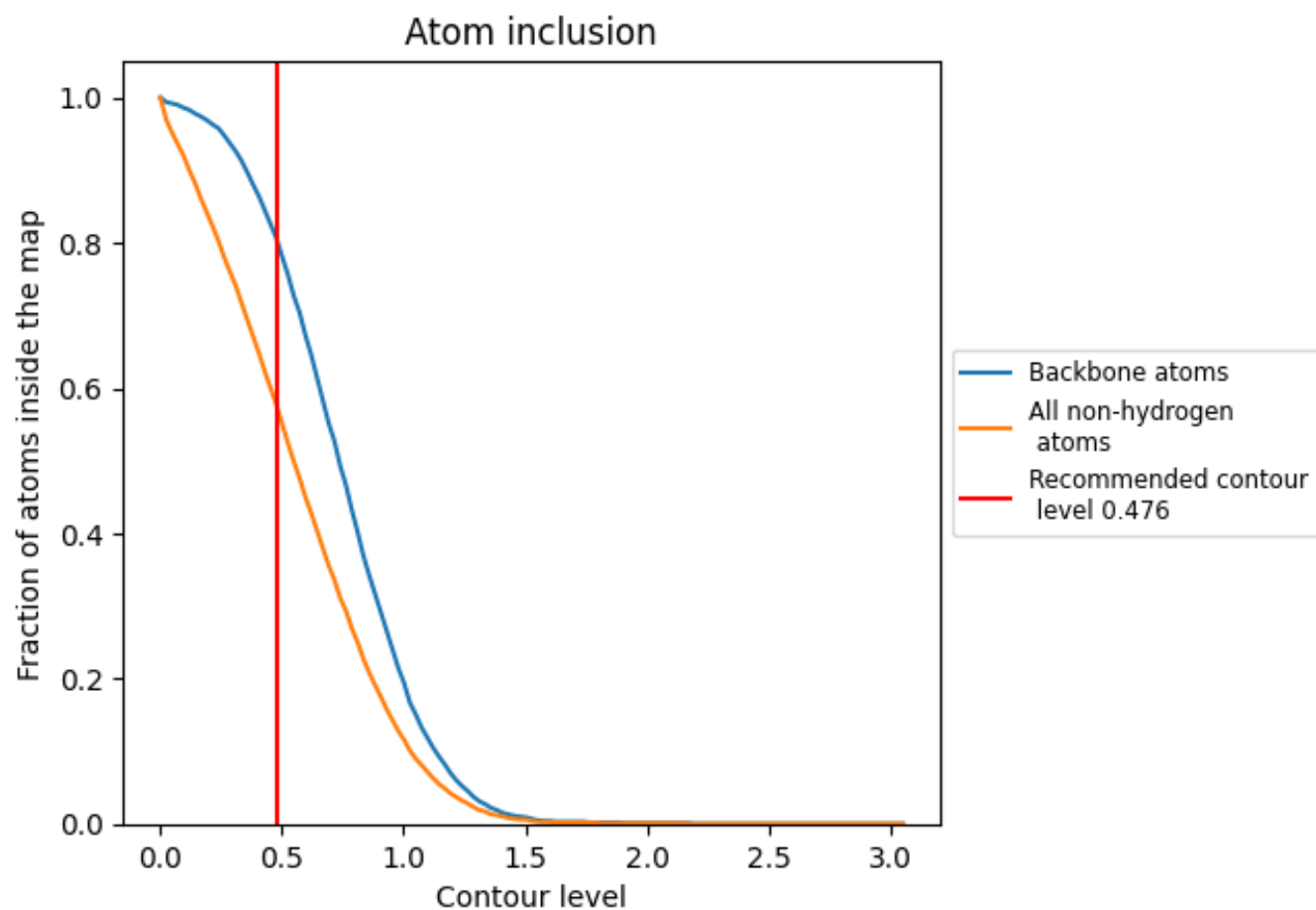
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.476).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.476) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5780	 0.3230
B	 0.5350	 0.2980
C	 0.5920	 0.3420
D	 0.5650	 0.3490
E	 0.6170	 0.3960
F	 0.6630	 0.3500
G	 0.5930	 0.3520
H	 0.6180	 0.2540
L	 0.5190	 0.2770
M	 0.5340	 0.3120
N	 0.5210	 0.2660

